Fig. 1A

```
1     GTCGACCCAC GCGTCCGAGA AGAAAATCCT AGATTTCTCC GTCTCTCTAA TTTCCTTTCT

61    CTCTCAAGCT TCTCAGAAAG TCTGACACTT TCGAGAATCT AATCTCCAAA TTTCTTGTCT

121   TTTTGGAGAA GGAATCGAAT T ATG TAC AAG GAA CGT AGT GGA GGA GGT GGT GGT GGG TCA
                             Met Tyr Lys Glu Arg Ser Gly Gly Gly Gly Gly Gly Ser      13

181   TCG AGA TCA GAG ATC CTC GGT GGA GCT ATT GAT CGG AAA CGA ATC AAC GAT GCA CTC AAT
      Ser Arg Ser Glu Ile Leu Gly Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu Asn  33

241   AAG AAA CTA GAG AAA TCT TCA ACT TCC ACC ACC ACA TCT AGG GTT TTC TCT TCT AAA GAC
      Lys Lys Leu Glu Lys Ser Ser Thr Ser Thr Thr Thr Ser Arg Val Phe Ser Ser Lys Asp  53

301   AAA GAT CCC TTT TCC TTC ACA TCT ACT AAA ACT CAG CTT CCT GAT GTG GAA TCG GAA ACT
      Lys Asp Pro Phe Ser Phe Thr Ser Thr Lys Thr Gln Leu Pro Asp Val Glu Ser Glu Thr  73

361   GAT AGT GAA GGG TCT GAT GTG AGT GGA TCG GAG GGT GAT GAT ACG TCG TGG ATC TCT TGG
      Asp Ser Glu Gly Ser Asp Val Ser Gly Ser Glu Gly Asp Asp Thr Ser Trp Ile Ser Trp  93

421   TTT TGT AAT TTG AGA GGG AAT GAT TTC TTC TGT GAA GTC GAT GAA GAT TAT ATT CAA GAT
      Phe Cys Asn Leu Arg Gly Asn Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp  113

481   GAT TTC AAT CTT TGT GGT TTA AGT GGT CAA GTC CCT TAC TAT GAT TAT GCA CTT GAT CTC
      Asp Phe Asn Leu Cys Gly Leu Ser Gly Gln Val Pro Tyr Tyr Asp tyr Ala Leu Asp Leu  133

541   ATT TTA GAT GTT GAT GCT TCC AAC AGT GAG ATG TTT ACT GAT GAA CAG CAT GAA ATG GTG
      Ile Leu Asp Val Asp Ala Ser Asn Ser Glu Met Phe Thr Asp Glu Gln His Glu Met Val  153

601   GAA TCA GCT GCT GAG ATG CTA TAT GGT CTT ATT CAT GTT CGT TAC ATT TTG ACT ACT AAA
      Glu Ser Ala Ala Glu Met Leu Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys  173

661   GGA ATG GCT GCA ATG ACT GAG AAG TAC AAG AAC TGT GAT TTC GGG AGA TGC CCG AGA GTT
      Gly Met Ala Ala Met Thr Glu Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg Val  193

721   TTC TGT TGC GGT CAG TCT TGT CTT CCA GTT GGA CAA TCC GAT ATC CCG AGA TCG AGT ACT
      Phe Cys Cys Gly Gln Ser Cys Leu Pro Val Gly Gln Ser Asp Ile Pro Arg Ser Ser Thr  213

781   GTG AAG ATA TAC TGC CCT AAA TGC GAG GAT ATA TCT TAC CCG CGA TCT AAA TTC CAA GGC
      Val Lys Ile Tyr Cys Pro Lys Cys Glu Asp Ile Ser Tyr Pro Arg Ser Lys Phe Gln Gly  233

841   AAT ATT GAT GGA GCG TAC TTT GGA ACC ACA TTC CCT CAC TTG TTC TTG ATG ACT TAC GGG
      Asn Ile Asp Gly Ala Tyr Phe Gly Thr Thr Phe Pro His Leu Phe Leu Met Thr Tyr Gly  253

901   AAC TTA AAG CCG CAG AAG CCT ACT CAA AGC TAT GTC CCA AAA ATC TTT GGC TTC AAG GTA
      Asn Leu Lys Pro Gln Lys Pro Thr Gln Ser Tyr Val Pro Lys Ile Phe Gly Phe Lys Val  273

960   CAC AAA CCA TGATACTAGT GCTCTGCATT CTCAATGGTG ATACATTTAG TGGCTCTGTA
      His Lys Pro                                                                    276

1020  ATTGCATCCG GATGAGCAAC TGAAACGATA GCTGCGGTGA CTGGAGCATA CATCAACCAT T
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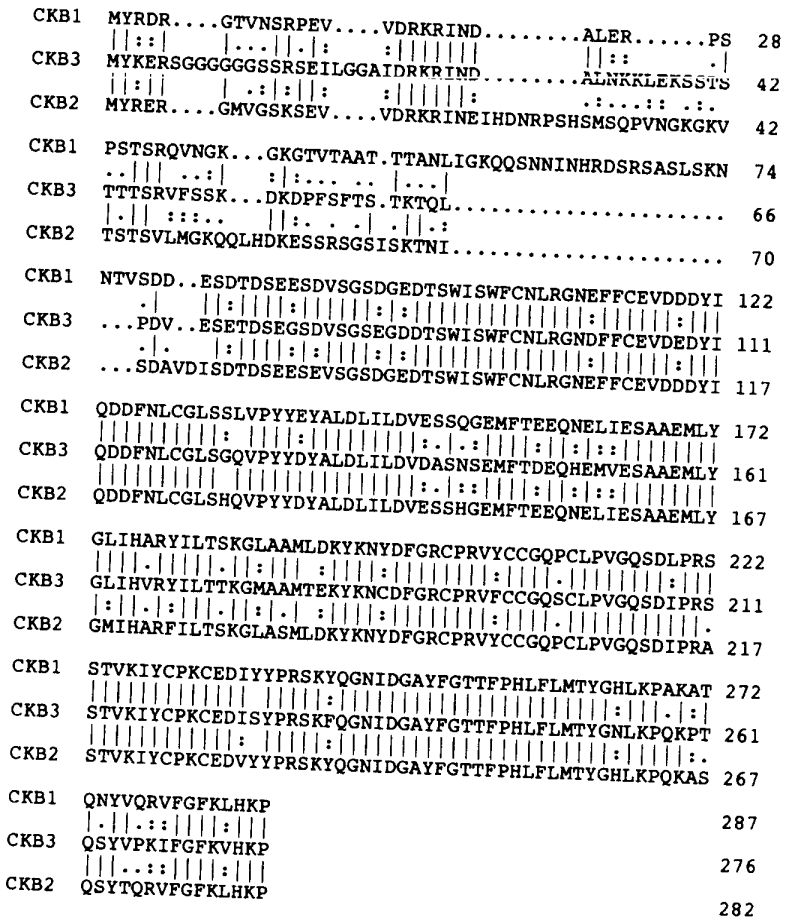
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CKB3 MYKERSGGGGGGSSRSEILGGAIDRKRIND.....ALNKKLEKSSTS 42
CKB2 MYRER....GMVGSKSEV....VDRKRINEIHDNRPSHSMSQPVNGKGKV 42
CKB1 PSTSRQVNGK...GKGTVTAAT.TTANLIGKQQSNNINHRDSRSASLSKN 74
CKB3 TTTSRVFSSK...DKDPFSFTS.TKTQL..... 66
CKB2 TSTSVLMGKQQLHDKESSRSGSISKTNI..... 70
CKB1 NTVSDD..ESDTDSEESDVSGSDGEDTSWISWFCNLRGNEFFCEVDDDYI 122
CKB3 ...PDV..ESETDSEGSDVSGSEGDDTSWISWFCNLRGNDFFCEVDEDYI 111
CKB2 ...SDAVDISDTDSEESEVSGSDGEDTSWISWFCNLRGNEFFCEVDDDYI 117
CKB1 QDDFNLCGLSSLVPYYEYALDLILDVESSQGEMFTEEQNELIESAAEMLY 172
CKB3 QDDFNLCGLSGQVPYYDYALDLILDVDASNSEMFTDEQHEMVESAAEMLY 161
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CKB1 GLIHARYILTSKGLAAMLDKYKNYDFGRCPRVYCCGQPCLPVGQSDLPRS 222
CKB3 GLIHVRYILTTKGMAAMTEKYKNCDFGRCPRVFCCGQSCLPVGQSDIPRS 211
CKB2 GMIHARFILTSKGLASMLDKYKNYDFGRCPRVYCCGQPCLPVGQSDIPRA 217
CKB1 STVKIYCPKCEDIYYPRSKYQGNIDGAYFGTTFPHLFLMTYGHLKPAKAT 272
CKB3 STVKIYCPKCEDISYPRSKFQGNIDGAYFGTTFPHLFLMTYGNLKPQKPT 261
CKB2 STVKIYCPKCEDVYYPRSKYQGNIDGAYFGTTFPHLFLMTYGHLKPQKAS 267
CKB1 QNYVQRVFGFKLHKP 287
CKB3 QSYVPKIFGFKVHKP 276
CKB2 QSYTQRVFGFKLHKP 282

Fig. 1B

Fig. 2

SEQ. I.D. No. 1

GTCGACCCAC GCGTCCGAGA AGAAAACCCT AGATTTCTCC GTCTCTCTAA TTTCCTTTCT 60

CTCTCAAGCT TCTCAGAAAG TCTGACACTT TCGAGAATCT AATCTCCAAA TTTCTTGTCT 120

TTTTGGAGAA GGAATCGAAT TATGTACAAG GAACGTAGTG GAGGAGGTGG TGGTGGGTCA 180

TCGAGATCAG AGATCCTCGG TGGAGCTATT GATCGGAAAC GAATCAACGA TGCACTCAAT 240

AAGAAACTAG AGAAATCTTC AACTTCCACC ACCACATCTA GGGTTTTCTC TTCTAAAGAC 300

AAAGATCCCT TTTCCTTCAC ATCTACTAAA ACTCAGCTTC CTGATGTGGA ATCGGAAACT 360

GATAGTGAAG GGTCTGATGT GAGTGGATCG GAGGGTGATG ATACGTCGTG GATCTCTTGG 420

TTTTGTAATT TGAGAGGGAA TGATTTCTTC TGTGAAGTCG ATGAAGATTA TATTCAAGAT 480

GATTTCAATC TTTGTGGTTT AAGTGGTCAA GTCCCTTACT ATGATTATGC ACTTGATCTC 540

ATTTTAGATG TTGATGCTTC CAACAGTGAG ATGTTTACTG ATGAACAGCA TGAAATGGTG 600

GAATCAGCTG CTGAGATGCT ATATGGTCTT ATTCATGTTC GTTACATTTT GACTACTAAA 660

GGAATGGCTG CAATGACTGA GAAGTACAAG AACTGTGATT TCGGGAGATG CCCGAGAGTT 720

TTCTGTTGCG GTCAGTCTTG TCTTCCAGTT GGACAATCCG ATATCCCGAG ATCGAGTACT 780

GTGAAGATAT ACTGCCCTAA ATGCGAGGAT ATATCTTACC CGCGATCTAA ATTCCAAGGC 841

AATATTGATG GAGCGTACTT TGGAACCACA TTCCCTCACT TGTTCTTGAT GACTTACGGG 900

AACTTAAAGC CGCAGAAGCC TACTCAAAGC TATGTCCCAA AAATCTTTGG CTTCAAGGTA 961

CACAAACCAT GATACTAGTG CTCTGCATTC TCAATGGTGA TACATTTAGT GGCTCTGTAA 1020

TTGCATCCGG ATGAGCAACT GAAACGATAG CTGCGGTGAC TGGAGCATAC ATCAACCATT 1080

Fig. 3

SEQ. I.D. No. 2

Met Tyr Lys Glu Arg Ser Gly Gly Gly Gly Gly Gly Ser Ser Arg Ser Glu Ile Leu Gly 20

Gly Ala Ile Asp Arg Lys Arg Ile Asn Asp Ala Leu Asn Lys Lys Leu Glu Lys Ser Ser 40

Thr Ser Thr Thr Thr Ser Arg Val Phe Ser Ser Lys Asp Lys Asp Pro Phe Ser Phe Thr 60

Ser Thr Lys Thr Gln Leu Pro Asp Val Glu Ser Glu Thr Asp Ser Glu Gly Ser Asp Val 80

Ser Gly Ser Glu Gly Asp Asp Thr Ser Trp Ile Ser Trp Phe Cys Asn Leu Arg Gly Asn 100

Asp Phe Phe Cys Glu Val Asp Glu Asp Tyr Ile Gln Asp Asp Phe Asn Leu Cys Gly Leu 120

Ser Gly Gln Val Pro Tyr Tyr Asp Tyr Ala Leu Asp Leu Ile Leu Asp Val Asp Ala Ser 140

Asn Ser Glu Met Phe Thr Asp Glu Gln His Glu Met Val Glu Ser Ala Ala Glu Met Leu 160

Tyr Gly Leu Ile His Val Arg Tyr Ile Leu Thr Thr Lys Gly Met Ala Ala Met Thr Glu 180

Lys Tyr Lys Asn Cys Asp Phe Gly Arg Cys Pro Arg Val Phe Cys Cys Gly Gln Ser Cys 200

Leu Pro Val Gly Gln Ser Asp Ile Pro Arg Ser Ser Thr Val Lys Ile Tyr Cys Pro Lys 220

Cys Glu Asp Ile Ser Tyr Pro Arg Ser Lys Phe Gln Gly Asn Ile Asp Gly Ala Tyr Phe 240

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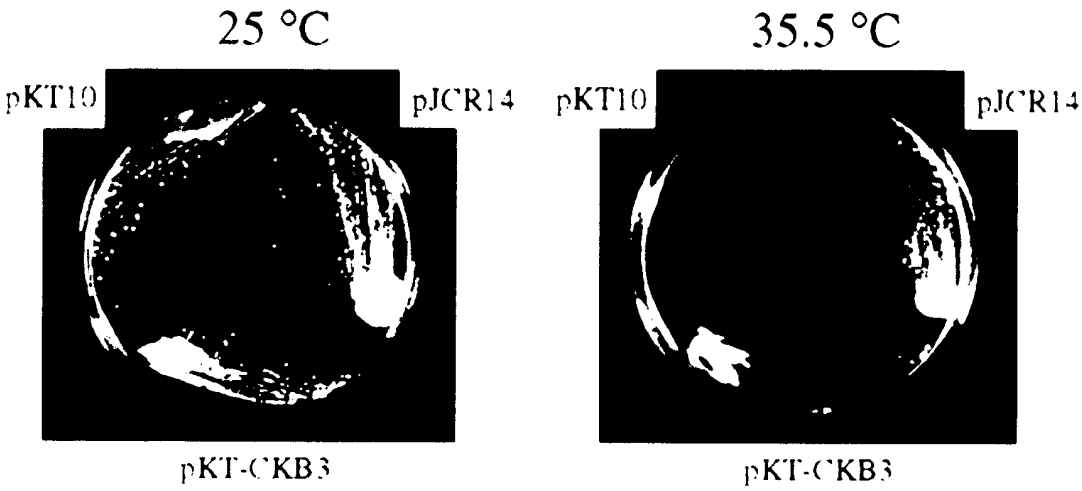

Fig. 4

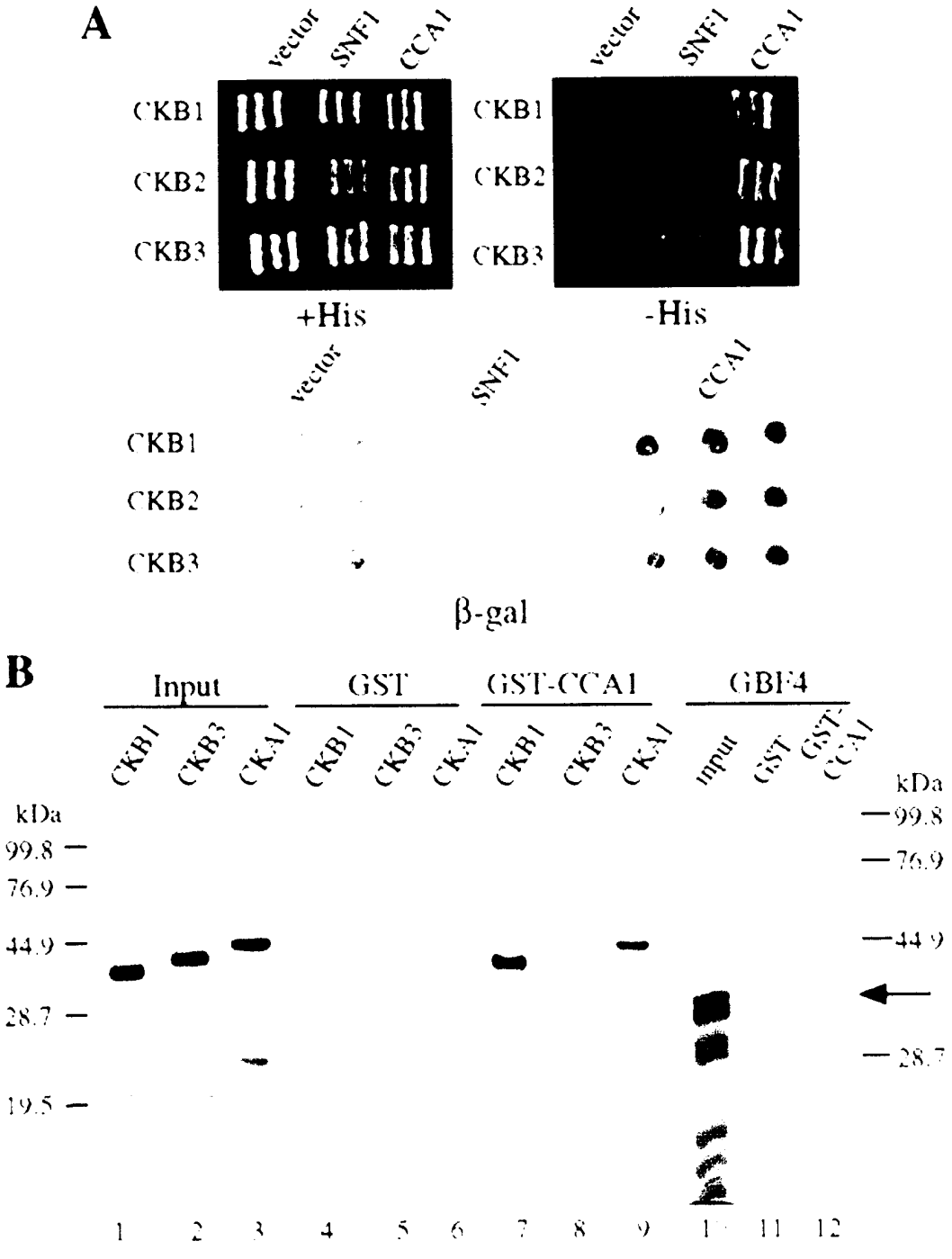
A
vector
SNF1
CCA1
CKB1
CKB2
CKB3
+His
-His
β-gal
B
Input
GST
GST-CCA1
GBF4
CKB1
CKB3
CKA1
input
GST
GST-CCA1
kDa
99.8
76.9
44.9
28.7
19.5
1
2
3
4
5
6
7
8
9
10
11
12

Fig. 5

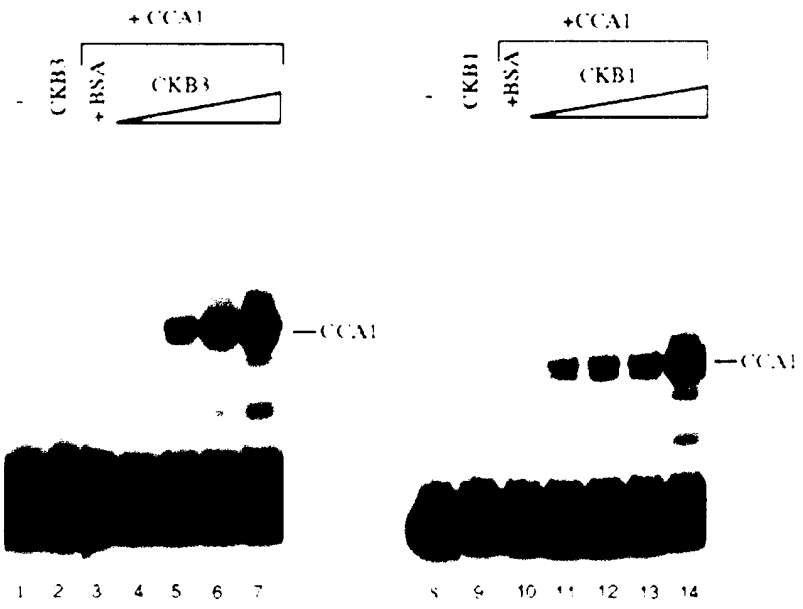
+CCA1
CKB3
+BSA
CKB3
+CCA1
CKB1
+BSA
CKB1
—CCA1
—CCA1
1 2 3 4 5 6 7
8 9 10 11 12 13 14

Fig. 6

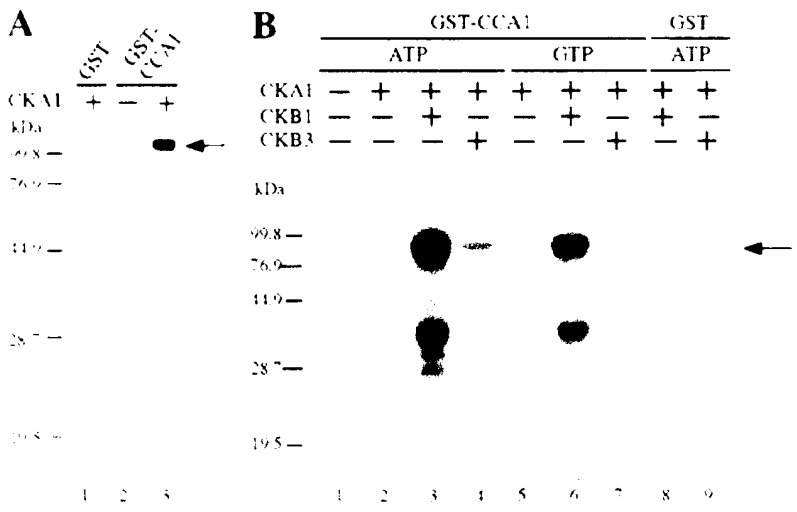
A
GST
GST-CCA1
CKA1 + − +
kDa
99.8
76.9
44.9
28.7
19.5
1 2 3
B
GST-CCA1
GST
ATP
GTP
ATP
CKA1 − + + + + + + + +
CKB1 − − + − − + − + −
CKB3 − − − + − − + − +
kDa
99.8
76.9
44.9
28.7
19.5
1 2 3 4 5 6 7 8 9

Fig. 7

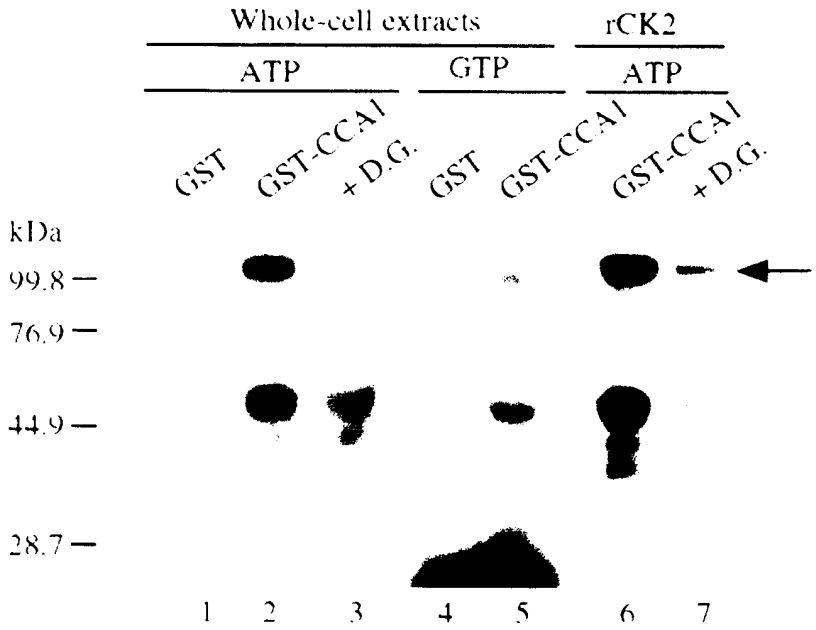
Whole-cell extracts
rCK2
ATP
GTP
ATP
GST
GST-CCA1
+D.G.
GST
GST-CCA1
GST-CCA1
+D.G.
kDa
99.8
76.9
44.9
28.7
1
2
3
4
5
6
7

Fig. 8

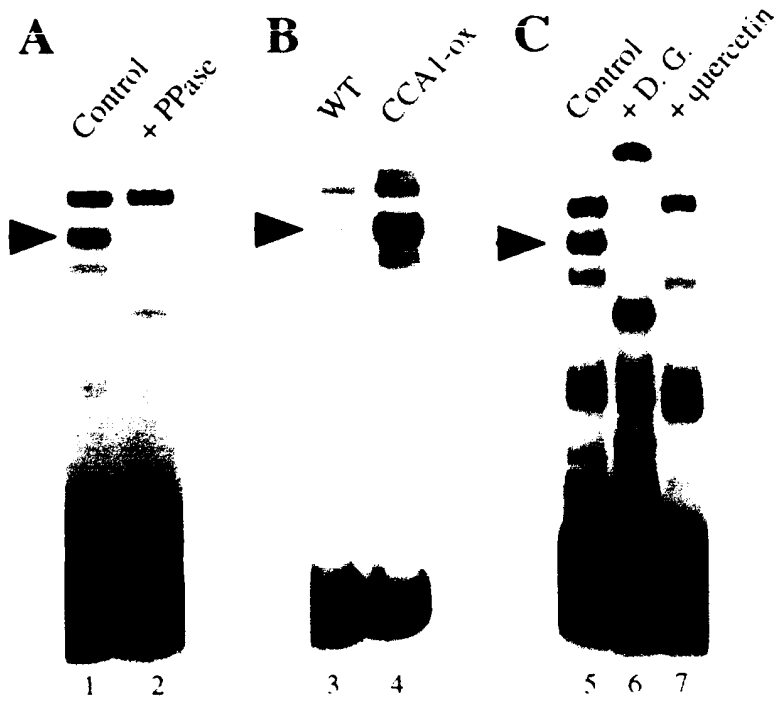

Fig. 9

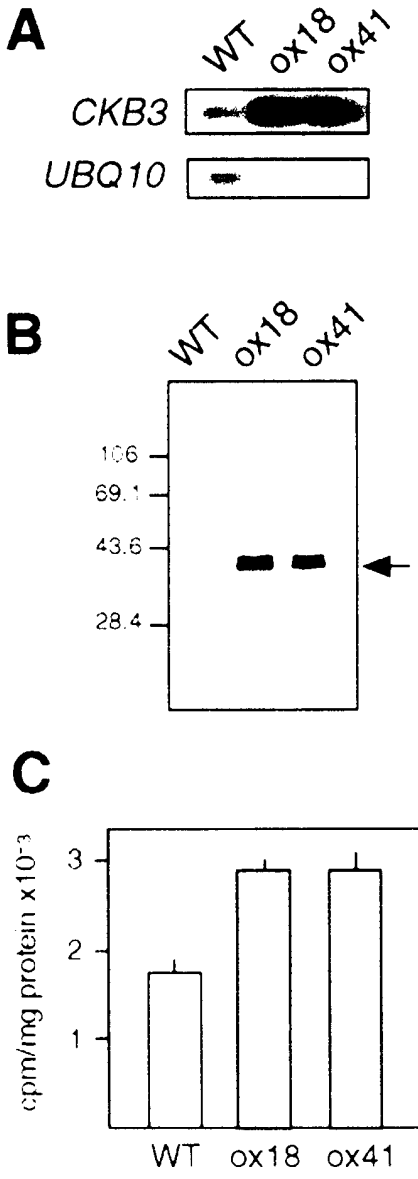
A
WT
ox18
ox41
CKB3
UBQ10
B
WT
ox18
ox41
106
69.1
43.6
28.4
C
cpm/mg protein x10⁻³
3
2
1
WT
ox18
ox41

Fig. 10

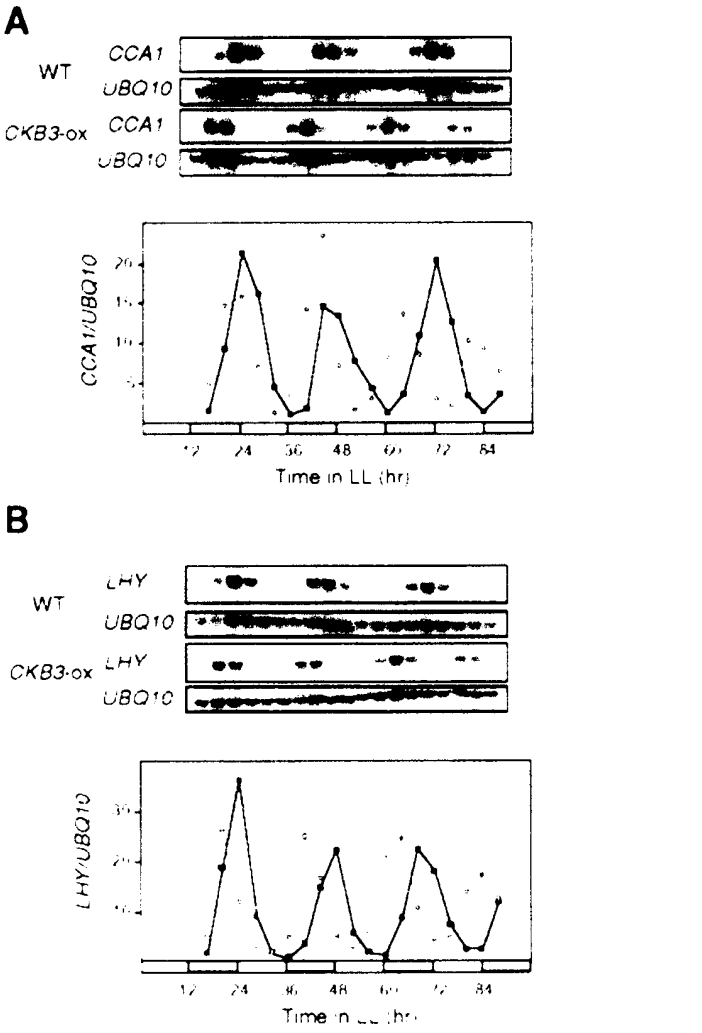
A
WT
CCA1
UBQ10
CKB3-ox
CCA1
UBQ10
CCA1/UBQ10
Time in LL (hr)
B
WT
LHY
UBQ10
CKB3-ox
LHY
UBQ10
LHY/UBQ10
C
WT
CKB3-ox

Fig. 11

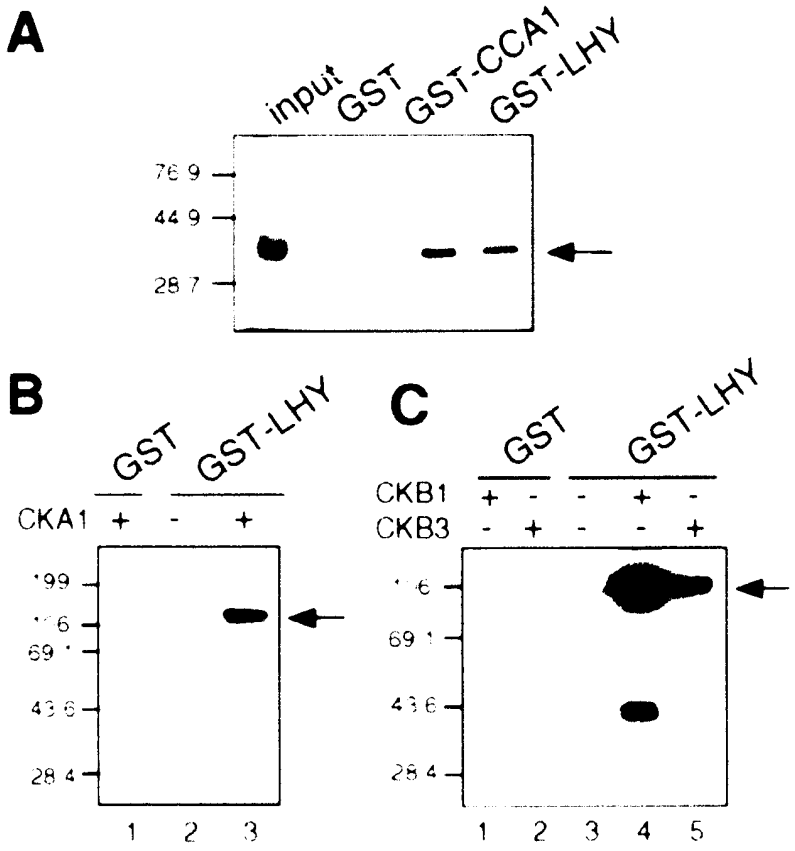
A
input
GST
GST-CCA1
GST-LHY
76.9
44.9
28.7
B
GST
GST-LHY
CKA1 + - +
69.1
43.6
28.4
1 2 3
C
GST
GST-LHY
CKB1 + - - + -
CKB3 - + - - +
69.1
43.6
28.4
1 2 3 4 5

Fig. 12

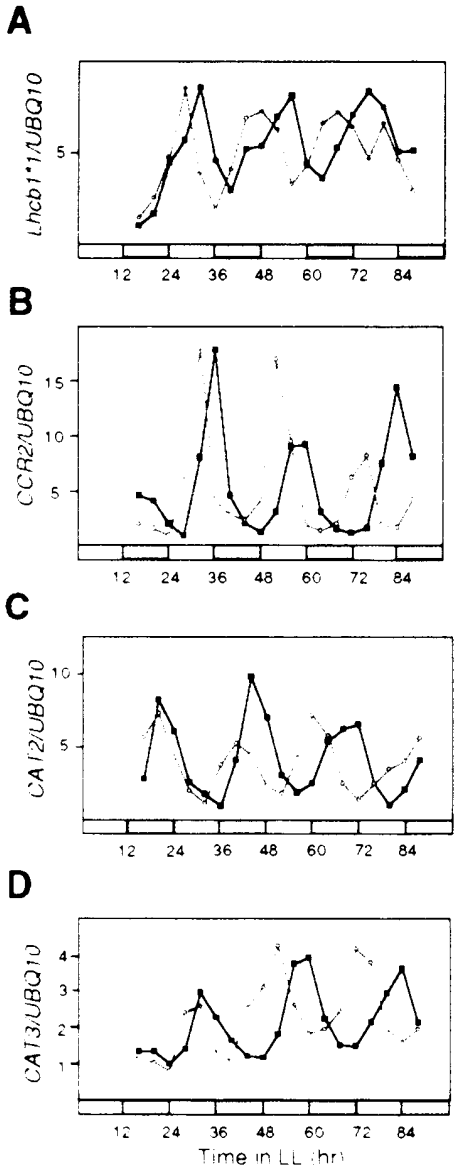
A
Lhcb1*1/UBQ10
5
12 24 36 48 60 72 84
B
CCR2/UBQ10
15
10
5
12 24 36 48 60 72 84
C
CAT2/UBQ10
10
5
12 24 36 48 60 72 84
D
CAT3/UBQ10
4
3
2
1
12 24 36 48 60 72 84
Time in LL (hr)

Fig. 13